

RAW SEQUENCE LISTING

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Application Serial Number: 10/511,269
Source: PCF
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PCT

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/511,269

DATE: 04/14/2006

TIME: 11:14:33

Input Set : F:\260276US0PCT.txt

Output Set: N:\CRF4\04142006\J511269.raw

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3 <110> APPLICANT: MORI, HIROSHI
5 <120> TITLE OF INVENTION: GAMMA-SECRETASE INHIBITORS
7 <130> FILE REFERENCE: 260276US0PCT
9 <140> CURRENT APPLICATION NUMBER: 10/511,269
10 <141> CURRENT FILING DATE: 2004-10-20
12 <150> PRIOR APPLICATION NUMBER: PCT/JP03/050117
13 <151> PRIOR FILING DATE: 2003-04-18
15 <150> PRIOR APPLICATION NUMBER: JP2002-121983
16 <151> PRIOR FILING DATE: 2002-04-24
18 <160> NUMBER OF SEQ ID NOS: 13
20 <170> SOFTWARE: PatentIn version 3.3
22 <210> SEQ ID NO: 1
23 <211> LENGTH: 17
24 <212> TYPE: PRT
25 <213> ORGANISM: Homo sapiens
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33 Lys
37 <210> SEQ ID NO: 2
38 <211> LENGTH: 6
39 <212> TYPE: PRT
40 <213> ORGANISM: Homo sapiens
42 <400> SEQUENCE: 2
44 Ile Thr Leu Val Met Leu
45 1          5
48 <210> SEQ ID NO: 3
49 <211> LENGTH: 4
50 <212> TYPE: PRT
51 <213> ORGANISM: Homo sapiens
53 <400> SEQUENCE: 3
55 Leu Val Met Leu
56 1
59 <210> SEQ ID NO: 4
60 <211> LENGTH: 4
61 <212> TYPE: PRT
62 <213> ORGANISM: Homo sapiens
64 <400> SEQUENCE: 4
66 Thr Leu Val Met
67 1
70 <210> SEQ ID NO: 5
71 <211> LENGTH: 11
72 <212> TYPE: PRT

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78 1 5 10
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82 <211> LENGTH: 2088
83 <212> TYPE: DNA
84 <213> ORGANISM: Homo sapiens
87 <220> FEATURE:
88 <221> NAME/KEY: CDS
89 <222> LOCATION: (1)..(2088)
91 <400> SEQUENCE: 6
92 atg ctg ccc ggt ttg gca ctg ctc ctg ctg gcc gcc tgg acg gct cgg 48
93 Met Leu Pro Gly Leu Ala Leu Leu Leu Leu Ala Ala Trp Thr Ala Arg
94 1 5 10 15
96 gcg ctg gag gta ccc act gat ggt aat gct ggc ctg ctg gct gaa ccc 96
97 Ala Leu Glu Val Pro Thr Asp Gly Asn Ala Gly Leu Leu Ala Glu Pro
98 20 25 30
100 cag att gcc atg ttc tgt ggc aga ctg aac atg cac atg aat gtc cag 144
101 Gln Ile Ala Met Phe Cys Gly Arg Leu Asn Met His Met Asn Val Gln
102 35 40 45
104 aat ggg aag tgg gat tca gat cca tca ggg acc aaa acc tgc att gat 192
105 Asn Gly Lys Trp Asp Ser Asp Pro Ser Gly Thr Lys Thr Cys Ile Asp
106 50 55 60
108 acc aag gaa ggc atc ctg cag tat tgc caa gaa gtc tac cct gaa ctg 240
109 Thr Lys Glu Gly Ile Leu Gln Tyr Cys Gln Glu Val Tyr Pro Glu Leu
110 65 70 75 80
112 cag atc acc aat gtg gta gaa gcc aac caa cca gtg acc atc cag aac 288
113 Gln Ile Thr Asn Val Val Glu Ala Asn Gln Pro Val Thr Ile Gln Asn
114 85 90 95
116 tgg tgc aag cgg ggc cgc aag cag tgc aag acc cat ccc cac ttt gtg 336
117 Trp Cys Lys Arg Gly Arg Lys Gln Cys Lys Thr His Pro His Phe Val
118 100 105 110
120 att ccc tac cgc tgc tta gtt ggt gag ttt gta agt gat gcc ctt ctc 384
121 Ile Pro Tyr Arg Cys Leu Val Gly Glu Phe Val Ser Asp Ala Leu Leu
122 115 120 125
124 gtt cct gac aag tgc aaa ttc tta cac cag gag agg atg gat gtt tgc 432
125 Val Pro Asp Lys Cys Lys Phe Leu His Gln Glu Arg Met Asp Val Cys
126 130 135 140
128 gaa act cat ctt cac tgg cac acc gtc gcc aaa gag aca tgc agt gag 480
129 Glu Thr His Leu His Trp His Thr Val Ala Lys Glu Thr Cys Ser Glu
130 145 150 155 160
132 aag agt acc aac ttg cat gac tac ggc atg ttg ctg ccc tgc gga att 528
133 Lys Ser Thr Asn Leu His Asp Tyr Gly Met Leu Leu Pro Cys Gly Ile
134 165 170 175
136 gac aag ttc cga ggg gta gag ttt gtg tgt tgc cca ctg gct gaa gaa 576
137 Asp Lys Phe Arg Gly Val Glu Phe Val Cys Cys Pro Leu Ala Glu Glu
138 180 185 190
140 agt gac aat gtg gat tct gct gat gcg gag gag gat gac tcg gat gtc 624

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141	Ser	Asp	Asn	Val	Asp	Ser	Ala	Asp	Ala	Glu	Glu	Asp	Asp	Ser	Asp	Val	
142			195					200					205				
144	tgg	tgg	ggc	gga	gca	gac	aca	gac	tat	gca	gat	ggg	agt	gaa	gac	aaa	672
145	Trp	Trp	Gly	Gly	Ala	Asp	Thr	Asp	Tyr	Ala	Asp	Gly	Ser	Glu	Asp	Lys	
146		210					215					220					
148	gta	gta	gaa	gta	gca	gag	gag	gaa	gaa	gtg	gct	gag	gtg	gaa	gaa	gaa	720
149	Val	Val	Glu	Val	Ala	Glu	Glu	Glu	Glu	Val	Ala	Glu	Val	Glu	Glu	Glu	
150	225					230					235					240	
152	gaa	gcc	gat	gat	gac	gag	gac	gat	gag	gat	ggg	gat	gag	gta	gag	gaa	768
153	Glu	Ala	Asp	Asp	Asp	Glu	Asp	Asp	Glu	Asp	Gly	Asp	Glu	Val	Glu	Glu	
154					245					250					255		
156	gag	gct	gag	gaa	ccc	tac	gaa	gaa	gcc	aca	gag	aga	acc	acc	agc	att	816
157	Glu	Ala	Glu	Glu	Pro	Tyr	Glu	Glu	Ala	Thr	Glu	Arg	Thr	Thr	Ser	Ile	
158			260						265				270				
160	gcc	acc	acc	acc	acc	acc	acc	aca	gag	tct	gtg	gaa	gag	gtg	gtt	cga	864
161	Ala	Thr	Thr	Thr	Thr	Thr	Thr	Thr	Glu	Ser	Val	Glu	Glu	Val	Val	Arg	
162			275					280				285					
164	gtt	cct	aca	aca	gca	gcc	agt	acc	cct	gat	gcc	gtt	gac	aag	tat	ctc	912
165	Val	Pro	Thr	Thr	Ala	Ala	Ser	Thr	Pro	Asp	Ala	Val	Asp	Lys	Tyr	Leu	
166		290					295				300						
168	gag	aca	cct	ggg	gat	gag	aat	gaa	cat	gcc	cat	ttc	cag	aaa	gcc	aaa	960
169	Glu	Thr	Pro	Gly	Asp	Glu	Asn	Glu	His	Ala	His	Phe	Gln	Lys	Ala	Lys	
170	305				310					315					320		
172	gag	agg	ctt	gag	gcc	aag	cac	cga	gag	aga	atg	tcc	cag	gtc	atg	aga	1008
173	Glu	Arg	Leu	Glu	Ala	Lys	His	Arg	Glu	Arg	Met	Ser	Gln	Val	Met	Arg	
174					325				330				335				
176	gaa	tgg	gaa	gag	gca	gaa	cgt	caa	gca	aag	aac	ttg	cct	aaa	gct	gat	1056
177	Glu	Trp	Glu	Glu	Ala	Glu	Arg	Gln	Ala	Lys	Asn	Leu	Pro	Lys	Ala	Asp	
178			340					345				350					
180	aag	aag	gca	gtt	atc	cag	cat	ttc	cag	gag	aaa	gtg	gaa	tct	ttg	gaa	1104
181	Lys	Lys	Ala	Val	Ile	Gln	His	Phe	Gln	Glu	Lys	Val	Glu	Ser	Leu	Glu	
182			355					360				365					
184	cag	gaa	gca	gcc	aac	gag	aga	cag	cag	ctg	gtg	gag	aca	cac	atg	gcc	1152
185	Gln	Glu	Ala	Ala	Asn	Glu	Arg	Gln	Gln	Leu	Val	Glu	Thr	His	Met	Ala	
186		370				375				380							
188	aga	gtg	gaa	gcc	atg	ctc	aat	gac	cgc	cgc	cgc	ctg	gcc	ctg	gag	aac	1200
189	Arg	Val	Glu	Ala	Met	Leu	Asn	Asp	Arg	Arg	Arg	Leu	Ala	Leu	Glu	Asn	
190	385				390				395			400					
192	tac	atc	acc	gct	ctg	cag	gct	gtt	cct	cct	cgg	cct	cgt	cac	gtg	ttc	1248
193	Tyr	Ile	Thr	Ala	Leu	Gln	Ala	Val	Pro	Pro	Arg	Pro	Arg	His	Val	Phe	
194			405					410				415					
196	aat	atg	cta	aag	aag	tat	gtc	cgc	gca	gaa	cag	aag	gac	aga	cag	cac	1296
197	Asn	Met	Leu	Lys	Lys	Tyr	Val	Arg	Ala	Glu	Gln	Lys	Asp	Arg	Gln	His	
198			420					425				430					
200	acc	cta	aag	cat	ttc	gag	cat	gtg	cgc	atg	gtg	gat	ccc	aag	aaa	gcc	1344
201	Thr	Leu	Lys	His	Phe	Glu	His	Val	Arg	Met	Val	Asp	Pro	Lys	Lys	Ala	
202			435					440				445					
204	gct	cag	atc	cgg	tcc	cag	gtt	atg	aca	cac	ctc	cgt	gtg	att	tat	gag	1392
205	Ala	Gln	Ile	Arg	Ser	Gln	Val	Met	Thr	His	Leu	Arg	Val	Ile	Tyr	Glu	

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206      450      455      460
208 cgc atg aat cag tct ctc tcc ctg ctc tac aac gtg cct gca gtg gcc      1440
209 Arg Met Asn Gln Ser Leu Ser Leu Leu Tyr Asn Val Pro Ala Val Ala
210 465      470      475      480
212 gag gag att cag gat gaa gtt gat gag ctg ctt cag aaa gag caa aac      1488
213 Glu Glu Ile Gln Asp Glu Val Asp Glu Leu Leu Gln Lys Glu Gln Asn
214      485      490      495
216 tat tca gat gac gtc ttg gcc aac atg att agt gaa cca agg atc agt      1536
217 Tyr Ser Asp Asp Val Leu Ala Asn Met Ile Ser Glu Pro Arg Ile Ser
218      500      505      510
220 tac gga aac gat gct ctc atg cca tct ttg acc gaa acg aaa acc acc      1584
221 Tyr Gly Asn Asp Ala Leu Met Pro Ser Leu Thr Glu Thr Lys Thr Thr
222      515      520      525
224 gtg gag ctc ctt ccc gtg aat gga gag ttc agc ctg gac gat ctc cag      1632
225 Val Glu Leu Leu Pro Val Asn Gly Glu Phe Ser Leu Asp Asp Leu Gln
226      530      535      540
228 ccg tgg cat tct ttt ggg gct gac tct gtg cca gcc aac aca gaa aac      1680
229 Pro Trp His Ser Phe Gly Ala Asp Ser Val Pro Ala Asn Thr Glu Asn
230 545      550      555      560
232 gaa gtt gag cct gtt gat gcc cgc cct gct gcc gac cga gga ctg acc      1728
233 Glu Val Glu Pro Val Asp Ala Arg Pro Ala Ala Asp Arg Gly Leu Thr
234      565      570      575
236 act cga cca ggt tct ggg ttg aca aat atc aag acg gag gag atc tct      1776
237 Thr Arg Pro Gly Ser Gly Leu Thr Asn Ile Lys Thr Glu Glu Ile Ser
238      580      585      590
240 gaa gtg aag atg gat gca gaa ttc cga cat gac tca gga tat gaa gtt      1824
241 Glu Val Lys Met Asp Ala Glu Phe Arg His Asp Ser Gly Tyr Glu Val
242      595      600      605
244 cat cat caa aaa ttg gtg ttc ttt gca gaa gat gtg ggt tca aac aaa      1872
245 His His Gln Lys Leu Val Phe Phe Ala Glu Asp Val Gly Ser Asn Lys
246      610      615      620
248 ggt gca atc att gga ctc atg gtg ggc ggt gtt gtc ata gcg aca gtg      1920
249 Gly Ala Ile Ile Gly Leu Met Val Gly Gly Val Val Ile Ala Thr Val
250 625      630      635      640
252 atc gtc atc acc ttg gtg atg ctg aag aag aaa cag tac aca tcc att      1968
253 Ile Val Ile Thr Leu Val Met Leu Lys Lys Lys Gln Tyr Thr Ser Ile
254      645      650      655
256 cat cat ggt gtg gtg gag gtt gac gcc gct gtc acc cca gag gag cgc      2016
257 His His Gly Val Val Glu Val Asp Ala Ala Val Thr Pro Glu Glu Arg
258      660      665      670
260 cac ctg tcc aag atg cag cag aac ggc tac gaa aat cca acc tac aag      2064
261 His Leu Ser Lys Met Gln Gln Asn Gly Tyr Glu Asn Pro Thr Tyr Lys
262      675      680      685
264 ttc ttt gag cag atg cag aac tag      2088
265 Phe Phe Glu Gln Met Gln Asn
266      690      695
269 <210> SEQ ID NO: 7
270 <211> LENGTH: 695
271 <212> TYPE: PRT

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272 <213> ORGANISM: Homo sapiens

274 <400> SEQUENCE: 7

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276 Met Leu Pro Gly Leu Ala Leu Leu Leu Leu Ala Ala Trp Thr Ala Arg
277 1          5          10          15
280 Ala Leu Glu Val Pro Thr Asp Gly Asn Ala Gly Leu Leu Ala Glu Pro
281          20          25          30
284 Gln Ile Ala Met Phe Cys Gly Arg Leu Asn Met His Met Asn Val Gln
285          35          40          45
288 Asn Gly Lys Trp Asp Ser Asp Pro Ser Gly Thr Lys Thr Cys Ile Asp
289          50          55          60
292 Thr Lys Glu Gly Ile Leu Gln Tyr Cys Gln Glu Val Tyr Pro Glu Leu
293 65          70          75          80
296 Gln Ile Thr Asn Val Val Glu Ala Asn Gln Pro Val Thr Ile Gln Asn
297          85          90          95
300 Trp Cys Lys Arg Gly Arg Lys Gln Cys Lys Thr His Pro His Phe Val
301          100          105          110
304 Ile Pro Tyr Arg Cys Leu Val Gly Glu Phe Val Ser Asp Ala Leu Leu
305          115          120          125
308 Val Pro Asp Lys Cys Lys Phe Leu His Gln Glu Arg Met Asp Val Cys
309          130          135          140
312 Glu Thr His Leu His Trp His Thr Val Ala Lys Glu Thr Cys Ser Glu
313 145          150          155          160
316 Lys Ser Thr Asn Leu His Asp Tyr Gly Met Leu Leu Pro Cys Gly Ile
317          165          170          175
320 Asp Lys Phe Arg Gly Val Glu Phe Val Cys Cys Pro Leu Ala Glu Glu
321          180          185          190
324 Ser Asp Asn Val Asp Ser Ala Asp Ala Glu Glu Asp Asp Ser Asp Val
325          195          200          205
328 Trp Trp Gly Gly Ala Asp Thr Asp Tyr Ala Asp Gly Ser Glu Asp Lys
329          210          215          220
332 Val Val Glu Val Ala Glu Glu Glu Glu Val Ala Glu Val Glu Glu Glu
333 225          230          235          240
336 Glu Ala Asp Asp Asp Glu Asp Asp Glu Asp Gly Asp Glu Val Glu Glu
337          245          250          255
340 Glu Ala Glu Glu Pro Tyr Glu Glu Ala Thr Glu Arg Thr Thr Ser Ile
341          260          265          270
344 Ala Thr Thr Thr Thr Thr Thr Thr Glu Ser Val Glu Glu Val Val Arg
345          275          280          285
348 Val Pro Thr Thr Ala Ala Ser Thr Pro Asp Ala Val Asp Lys Tyr Leu
349          290          295          300
352 Glu Thr Pro Gly Asp Glu Asn Glu His Ala His Phe Gln Lys Ala Lys
353 305          310          315          320
356 Glu Arg Leu Glu Ala Lys His Arg Glu Arg Met Ser Gln Val Met Arg
357          325          330          335
360 Glu Trp Glu Glu Ala Glu Arg Gln Ala Lys Asn Leu Pro Lys Ala Asp
361          340          345          350
364 Lys Lys Ala Val Ile Gln His Phe Gln Glu Lys Val Glu Ser Leu Glu
365          355          360          365
368 Gln Glu Ala Ala Asn Glu Arg Gln Gln Leu Val Glu Thr His Met Ala

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VERIFICATION SUMMARY

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